



APPENDIX Ia

```
*
1 MDRG-----SSRRRTGSRPSSH--GGGPAAAEEVRDAAAG
1 MDRGGAG-----SSRRRTGSRVSQ--GGGPKVEEDEVRDAAVS
1 MAILDSAGVTTVTENGGEFVDLRLRRRKSRSDSSNGLLLSGSDNNSPDDVVGAPADVR
1 MAILDSAGVTTVTENGGEFVDLRLRRRKSRSDSSNGLLLSGSDNNSPDDVVGAPADVR
1 MVGSDGDG-----DGGGG--EAHAGPRRRAGQLRG--RLRDEAAGSPPPRPRPRPR
1 MAISDEPESVATA-----LNHSSLRRRPSATSTAGLNFSPETTTDSSGDDDLAKDSGSD
1 MSKGNPDP-----HLPGSFLPSHGGPPPKPTPRTFRNLPSSSTHGPAPSVAAATAT
1
60

*
38 PDVGAAGDAPAPAP-----NKDGDAGVSGH-----WELRC-----HRLQDS
41 PDLGAGDAPAPAPAPAHTRDKDRTSVGDGY-----WDLRC-----HRLQDS
61 DRIDSVVNDDAQGTANLAGDNNGGDNNGGGRGGEGRGNADATFTYRPSVPAHRRARES
61 DRIDSVVNDDAQGTANLAGDNNGGDNNGGGRGGEGRGNADATFTYRPSVPAHRRARES
51 GG-----DSNGRSVLRPGGGGGRG-----GGGDFSAFT--F--RAAAPVHRKAKES
54 DSINS---DDAAVNSQQQNEK-----QDTDFSVLKFAYRPSVPAHRKVKES
55 TP-----PSASAAPLPPTVHGEAA-----HGA AAAARRDALL--PGVGAHRRRVKES
61
120

*** * * * * * * * * * * *
75 LFSDDSGFSNYR-GILNWCVVMLILSNARLFLLENLIKYGILVDPIQVVSLFLKDPHSWPA
84 LFSDDSGFSNYR-GILNWCVVMLILSNARLFLLENLIKYGILVDPIQVVSLFLKDPYSWPA
121 PLSSDAIFKQSHAGLFNLCVVVLI AVNSRLI IENLMKYGWLIRT--DFWFSSRSLRDWPL
121 PLSSDAIFKQSHAGLFNLCVVVLI AVNSRLI IENLMKYGWLIRT--DFWFSSRSLRDWPL
93 PLSSDAIFKQSHAGLFNLCVVVLI AVNSRLI IENLMKYGLLIRA--GFWFNDKSLRDWPL
97 PLSSDTIFRQSHAGLFNLCVVVLI AVNSRLI IENLMKYGLIKS--GFWFSSKSLRDWPL
100 PLSSDAIFRQSHAGLLNLCVVVLI AVNSRLI IENLMKYGLLIRA--GFWFSARSLGDWPL
121
180
```

[illegible]

	*	* * *	*
gi3746533_human	194	SLLALMAHTILFLKLFSDVNSWCR--RARAKAASAGKKASSAAAPHTVSYPDNLTYRD	
SEQ25_mouse	203	SVFALASYIMFLKLYSYRDVNLCWRQRRVKAKAVSTGKKVSGAAQAQSVPDNLTYRD	
SEQ26_Arab	239	VTLMMLT-CIVWLKLVSYAHTSY---DIRSLANAADKANP-----EVSYYV--SLKS	
SEQ2_Arab	239	VTLMMLT-CIVWLKLVSYAHTSY---DIRSLANAADKANP-----EVSYYV--SLKS	
SEQ14_rice	211	FLLIFIA-CIVWLKLVSAFTNH----DIRQLTMGGKKVDNELSTVDMDNLQPP---TLGN	
SEQ16_soy	215	VTLMLFS-CVVWLKLVSYAHTNY---DMRALTKLVEKGAEALLDTLNMDPYPNV---SFKS	
SEQ22_wheat	218	FVLMFIA-SITWLKLVSAFTNY---DIRILSQSIIEKGATHGSSIDEENIKGP---TINS	
	241	5	300

[illegible]

[illegible][illegible]

	* * *	*	*	*	*	*	*	*	*
gi3746533_human	432	TGMMAQIPLAWFVGRFFQGNYGNAAV-----WLSL-IIIGQPIAVLMYVDHYVYLNYEAPA							
SEQ25_mouse	443	TAMMAQVPLAWIVGRFFQGNYGNAAV-----WVTL-IIIGQPVALMYVDHYVYLNYDAPV							
SEQ26_Arab	464	LGIMFQVPLV-FITNVLQERF-GSTVGNMIFWFIFCIGQPMCULLY---YHDLMNRRKGS							
SEQ2_Arab	464	LGIMFQVPLV-FITNVLQERF-GSTVGNMIFWFIFCIGQPMCULLY---YHDLMNRRKGS							
SEQ14_rice	443	LGIMLQIPLI-VLTAYLKSKFRDTMVGNMIFWFFFCIYGQPMCLLLY---YHDVMNRIEK							
SEQ16_soy	447	GGIMFQVPLV-LITNVLQNKFNSMVGNMIFWFIFSILGQPMCULLY---YHDLMNRRKGK							
SEQ22_wheat	450	SGIMFQIPLL-FLTKYLQDKFKNTMVGNMIFWFFFFSIVGQPMCULLY---YHDVMNRQAQ							
	481								540

gi3746533_human	486 AEA	488
SEQ25_mouse	497 G-V	498
SEQ26_Arab	519 MS-	520
SEQ2_Arab	519 MS-	520
SEQ14_rice	499 AR-	500
SEQ16_soy	503 LD-	504
SEQ22_wheat	506 TNG	508
	541	